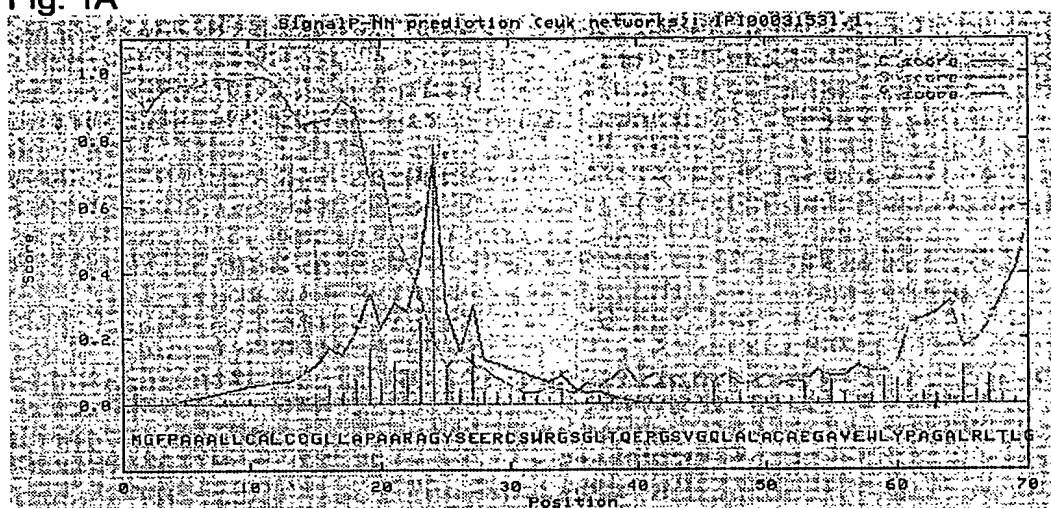


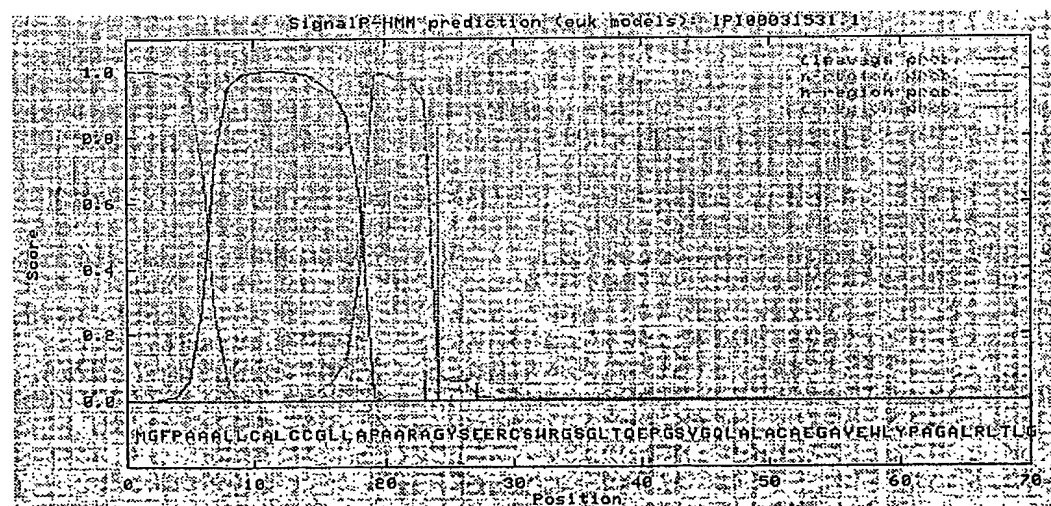
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Fig. 1A



```
>IPI00031531.1          length = 293
# Measure  Position  Value  Cutoff  signal peptide?
  max. C      24      0.785  0.33   YES
  max. Y      24      0.746  0.32   YES
  max. S      11      0.989  0.82   YES
  mean S      1-23     0.846  0.47   YES
# Most likely cleavage site between pos. 23 and 24: ARA-GY
```

Fig. 1B



```
>IPI00031531.1
Prediction: Signal peptide
Signal peptide probability: 1.000
Signal anchor probability: 0.000
Max cleavage site probability: 0.832 between pos. 23 and 24
```

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FIG. 2**human NsG33 (SEQ ID No 3)**

# Gene Ontology category	Odds
Signal_transducer	0.538
Receptor	0.433
Hormone	1.173
Structural_protein	0.168
Transporter	0.230
Ion_channel	0.372
Voltage-gated_ion_channel	0.130
Cation_channel	0.215
Transcription	0.294
Transcription_regulation	0.152
Stress_response	0.340
Immune_response	0.186
Growth_factor	2.083
Metal_ion_transport	0.020

human N-terminal peptide (SEQ ID No 19)

# Gene Ontology category	Odds
Signal_transducer	0.464
Receptor	0.296
Hormone	0.206
Structural_protein	0.987
Transporter	0.311
Ion_channel	0.147
Voltage-gated_ion_channel	0.157
Cation_channel	0.215
Transcription	0.311
Transcription_regulation	0.829
Stress_response	0.162
Immune_response	1.460
Growth_factor	8.142
Metal_ion_transport	0.061

human C-terminal peptide (SEQ ID No 5)

# Gene Ontology category	Odds
Signal_transducer	0.242
Receptor	0.038
Hormone	0.303
Structural_protein	0.096
Transporter	0.231
Ion_channel	0.185
Voltage-gated_ion_channel	0.191
Cation_channel	0.215
Transcription	0.312
Transcription_regulation	0.295
Stress_response	0.145
Immune_response	0.157
Growth_factor	7.963
Metal_ion_transport	0.020

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Fig 3a. CLUSTAL W (1.82) multiple sequence alignment

```

Mouse NsG33      HASAHASALLCALCCGLLAASAHAGYSEDRCSWRGSGLTQEPGSGVQLTLDCTEGAIEWL
Rat NsG33        ---MLVAALLCALCCGLLAASARAGYSEDRCSWRGSGLTQEPGSGVQLTLDCTEGAIEWL
Human NsG33      -MGFPAAALLCALCCGLLAPAARAGYSEERCSWRGSGLTQEPGSGVQLALACAEGAVEWL
                  .:*****.:*:*****:*****:*****:* *:***:***

Mouse NsG33      YPAGALRLTLGGPDGTRPSIVCLRPERPFAGAQVFAERMTGNLELLLAEGPDLAGGRCM
Rat NsG33        YPAGALRLTLGGSDPGTRPSIVCLRPTRPFAGAQVFAERMAGNLELLLAEGQGLAGGRCM
Human NsG33      YPAGALRLTLGGPDPRARPGIACLRPVRPFAGAQVFAERAGGALELLLAEGPGPAGGRCV
                  *****:* *:***.***** ***** * ***** . *****:

Mouse NsG33      RWGPRRRALFLQATPHRDISRRVAAFRFELHEDQRAEMSPQAQGLGVDGACRPCSDAEL
Rat NsG33        RWGPRRRALFLQATPHRDISRRVAAFQFELHEDQRAEMSPQAQGFVDGACRPCSDAEL
Human NsG33      RWGPRRRALFLQATPHQDISRRVAAFRFELREDGRPELPPQAHGLGVDGACRPCSDAEL
                  *****:*****:***:* *:*.***:*****:*****

Mouse NsG33      LLAactsdfvIHGTIHGVAHDTelQESVITVVVARVIRQTLPLFKESSEGGQGRASIRTL
Rat NsG33        LLTACTSDFVIHGTIHGVVHDMELQESVITVVATRVIRQTLPLFQESSEGRGQASVRTL
Human NsG33      LLAactsdfvIHGIHGVTHDVELQESVITVVAARVLRQTPPLFQAGRSGDQGLTSIRTP
                  *:***** *~~~*~ *****.:*:*** ***: * *~*~*:***

Mouse NsG33      LRCGVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFsRVYSaALTThLNpCEmALD
Rat NsG33        LRCGVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFsRVYSaALAAHLNpCEVALD
Human NsG33      LRCGVHPGPGTFLFMGWSRFGEARLGCAPRFQEFRRAYEAARAHLHPCEVALH
                  *****:***** ***** *~*~*~*:***:***.

```

Fig 3b. CLUSTAL W (1.82) multiple sequence alignment

```

Mouse      --MLVATLLCALCCGLLAASAHAGYSEDRCSWRGSGLTQEPGSGVQLTLDCTEGAIEWLY 58
Rat        --MLVAALLCALCCGLLAASARAGYSEDRCSWRGSGLTQEPGSGVQLTLDCTEGAIEWLY 58
Human      MGFPAAALLCALCCGLLAPAARAGYSEERCSWRGSGLTQEPGSGVQLALACAEGAVEWLY 60
            .:*****.:*:*****:*****:*****:* *:***:***

Mouse      PAGALRLTLGGPDGTRPSIVCLRPERPFAGAQVFAERMTGNLELLLAEGPDLAGGRCMR 118
Rat        PAGALRLTLGGSDPGTRPSIVCLRPTRPFAGAQVFAERMAGNLELLLAEGQGLAGGRCMR 118
Human      PAGALRLTLGGPDPRARPGIACLRPVRPFAGAQVFAERAGGALELLLAEGPGPAGGRCVR 120
            *****:* *:***.***** ***** * ***** . *****:

Mouse      WGPERRRALFLQATPHRDISRRVAAFRFELHEDQRAEMSPQAQGLGVDGACRPCSDAELL 178
Rat        WGPERRRALFLQATPHRDISRRVAAFQFELHEDQRAEMSPQAQGFVDGACRPCSDAELL 178
Human      WGPERRRALFLQATPHQDISRRVAAFRFELREDGRPELPPQAHGLGVDGACRPCSDAELL 180
            *****:*****:***:* *:*.***:*****:*****

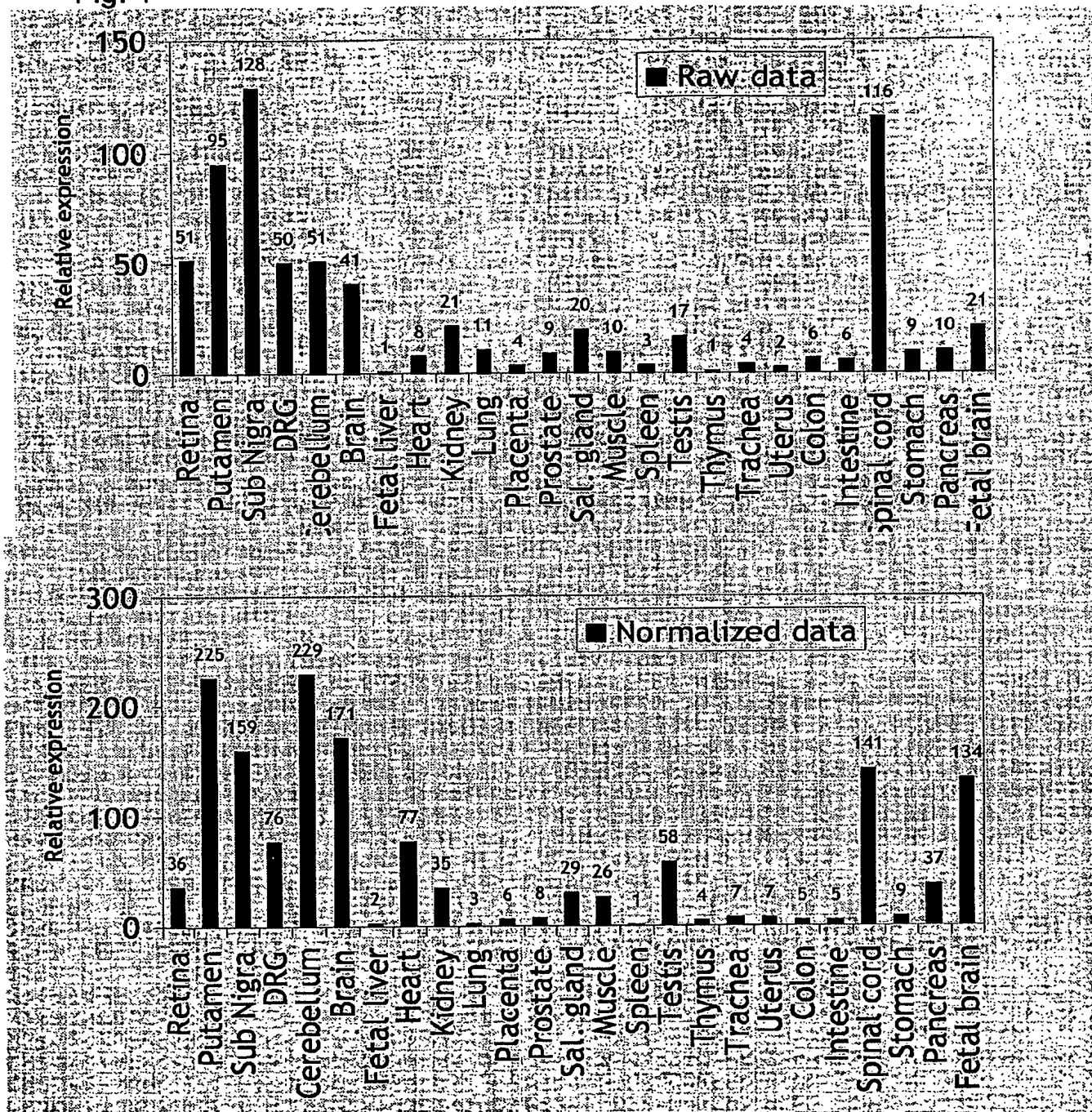
Mouse      LLAactsdfvIHGTIHGVAHDTelQESVITVVVARVIRQTLPLFKESSEGGQGRASIRTL 238
Rat        LTACTSDFVIHGTIHGVVHDMELQESVITVVATRVIRQTLPLFQESSEGRGQASVRTLL 238
Human      LLAactsdfvIHGIHGVTHDVELQESVITVVAARVLRQTPPLFQAGRSGDQGLTSIRTPL 240
            *:***** *~~~*~ *****.:*:*** ***: * *~*~*:***

Mouse      RCGVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFsRVYSaALTThLNpCEmALD 291
Rat        RCGVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFsRVYSaALAAHLNpCEVALD 291
Human      RCGVHPGPGTFLFMGWSRFGEARLGCAPRFQEFRRAYEAARAHLHPCEVALH 293
            ***~***~***** ***** *~*~*~*:***:***.

```

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Fig. 4



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scoring matrix: BLOSUM50, gap penalties: -12/-2
 42.3% identity; Global alignment score: 747

```

      10      20      30      40      50 *
Innog. MRGAARAAWGRAGQPWPRPPAPGPPPPPLPLLLLLLAGLLGGAG-AQYSSDRCSWKGSGL
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  -----MGFPAAALLCALCCGLLAPAAARAGYSEERCSSWRGSGL
                        10      20      30

      60      70      *  80      90      100      *110
Innog. THEAHRKEVEQVYLRCAAGAVEWMYPTGALIVNLR-PNTFSPARHLTVCI RSFTDSSGAN
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  TQEPGS--VGQIALACAEGAVEWLYPAGALRLTLGGPDPR--ARPGIACLRPVRPFAGAQ
      40      50      60      70      80      90

      120     130     140 *  150     160     170
Innog. IYLEKTG-ELRLLPDGDGRPGRVQC--FG-LEQGGLFVEATPQQDIGRRTTG FQYELVR
      .. :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  VFAERAGGALELLLAEGPG-PAGGRCVRWGPRERRALFLQATPHQDISRRVA AFRFELRE
      100     110     120     130     140     150

      180     190     200     210     220
Innog. RHRAS---DLHEL SAP--CRPCSDTEVLLAVCTSDFAVRGSIQQVTHEPERQDS AIHLRV
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  DGRPELPFQA HGLGVDGACRPCSDAELLAACTSDFVIHGIIHGVTHDVELQESVITVVA
      160     170*  *  180  *  190     200     210

      230     240     250     260     270     280
Innog. SRLYRQKSRVFEPVPEGDGHWQG--RVRTLLECGVRPGHGDFLFTGHMHFG EARLGCAPR
      .. :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  ARVLRQTTPPLFQAGRSGD---QGLTSIRTPLRCGVHPGPGTFLFMGWSRFGEARLGCAPR
      220     230     240 *  250     260     *

      290     300     *  310
Innog. FKDFQRM YRDAQERGLNPCEVGT D
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  FQEFRRAYEAARAAHLHPCEVALH
      270     280     290

```

Fig 5

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```

1  gcttcgcgg ggcggggcgg ccggcgcccc cggctgctcc cggcgccgcc cggacccggg ccccgccggg gcagcgtgg tgagagcccc gactccccgg
101 acgcgcggcg ccgtgccatg gggttccccg ccgcggcgct gctctgcgcg cttgtctgog gcctoctggc ccggtctgcc ccgcccggct actccgagga
    >>.....CDS.....
    m g f p a a a l l c a l c c g l l a p a a r a g y s e
201 gcgtgcagc tggaggggca gcgcctcac ccaggagccc ggcagcgtgg ggcagctggc cctggcctgt gcggaggggc cgttgtagtg gctgtaccgg
    >.....CDS.....
    e r c s w r g s g l t q e p g s v g q l a l a c a e g a v e w l y p
301 gctggggcgc tgcgcctgac cctggggcgc ccgcatccca gagcgcggcc cggcatgcc tgtctgcggc cgttcgggcc cttcgcgggc gccaggtct
    >.....CDS.....
    a g a l r l t l g p d p r a r p g i a c l r p v r p f a g a q v
401 tcgcggagcg cgcagggggc gccctggagc tgctgtggc gcagggcccg ggcggcgag ggggcgcgtg cgtgcgtgg ggtccccgcg agcgcgggc
    >.....CDS.....
    f a e r a g g a l e l l l a e g p g p a g g r c v r w g p r e r
501 cctcttctcg caggccacgc cgcaccagga catcagccgc cgcgtggcgg ccttcggcgt tgagctgcgc gaggaagggc gcccgagct gcccccgcag
    >.....CDS.....
    a l f l q a t p h q d i s r r v a a f r f e l r e d g r p e l p p q
601 gcccaaggtc tcggcgtaga cgtgcctgc aggcctgcga ggcacgtga gctgctctg gccgcctgca ccagcgactt cgtatccac gggatcatcc
    >.....CDS.....
    a h g l g v d g a c r p c s d a e l l l a a c t s d f v l h g i l
701 atggggtcac ccattgacgt gagctgcagg agtctgtcat cactgtgttg gccgcccgtg tcctccgcca gacaccgcg cgttccagg cggggcgatc
    >.....CDS.....
    h g v t h d v e l q e s v i t v v a a r v l r q t p p l f q a g r
801 cggggaccag gggctgacct ccattcgtac ccactgcgc tgtggcgtcc accggggccc aggcaccttc ctcttcattg gctggagccg ctttggggag
    >.....CDS.....
    s g d q g l t s i r t p l r c g v h p g p g t f l f m g w s r f g e
901 gcccggtgg gctgtgccc acgattccag gattccgcc gtgcctacga ggtgcccgt gctgcccacc tcaccccctg cgaggtggcg ctgcactgag
    >.....CDS.....
    a r l g c a p r f q e f r r a y e a a r a a h l h p c e v a l h -
1001 gggctgggtg ctggggaggg gctggtagga gggagggtgg gccactgct ttggaggtga tgggactatc ataagaact ctgttcacgc aaaaaaaaaa
1101 aaaaaaaaaa

```

Fig 6

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```

1  caacgcgtcc gccacgcgct ccgcgcttct ttgcgcgctc tgttgccgcc tctggccgc gtcgcctcac gctggctact cggaagaccg ctgcagctgg
>>.....CDS.....
>  h a s a h a s a l l c a l c c g l l a a s a h a g y s e d r c s w
101 aggggcagcg gtttgaccga ggagcctggc agcgtggggc agctgacct ggactgtact gagggcgcta togagtggct gtaccagct ggggcgctgc
>.....CDS.....
>  r g s g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l
201 gactgacct gggggccccc gatccgggca cagggccacg catcgtctgt ctggcccccag agcggccctt cgctggcgcc caggtctctcg ctgaacgtat
>.....CDS.....
>  r l t l g g p d p g t r p s i v c l r p e r p f a g a q v f a e r
301 gacgggcaat ctagagttgc tactggccga gggccgggac ctggctgggg gcgctgcat gcgctgggt cccgcgagc gcgagacct ttctctgcag
>.....CDS.....
>  m t g n l e l l l a e g p d l a g g r c m r w g p r e r a l f l q
401 gccacaccac accgcgcaat cagccgcaga gttgctgcct tccgttttga actgcacag gaccaacgtg cagaaatgc tcccaggct caaggtcttg
>.....CDS.....
>  a t p h r d i s r r v a a f r f e l h e d q r a e m s p q a q g l
501 gtgtggatgg tgcctgcagg ccctgcagtg atgcgagct cotcctggct gcatgcacca gtgattttgt gatccacggg accatccatg gggtcgcccc
>.....CDS.....
>  g v d g a c r p c s d a e l l l a a c t s d f v i h g t i h g v a
601 tgacacagag ctgcaagaat cagtcacac tgtgtgtgtt gctcgtgtca tccgccagac actgccactg ttcaagggaag ggaagctcga gggccaaaggc
>.....CDS.....
>  h d t e l q e s v i t v v v a r v i r q t l p l f k e g s s e g q g
701 cgggcctcca ttgtacctt gctgcgctgt ggtgtgcgtc ctggcccccag ctccttcctc ttcatgggtt ggagccgatt tggcgaagct tggctgggt
>.....CDS.....
>  r a s i r t l l r c g v r p g p g s f l f m g w s r f g e a w l g
801 gtgctcccc cttccaagag ttacgcccgtg tctattcagc tgctctcag acccatctca acccatgtga gatggcactg gactgagaga cctggggagca
>.....CDS.....
>  c a p r f q e f s r v y s a a l t t h l n p c e m a l d -
901 agccctggat ggaccttctt ctggagatgg ggtgttgggg aggtgtgatg gaggtgtggg gagaaggggt tggctcggat ggcctcctgg taccacagt
1001 gagctggtag aatactaagt aatctggacc ataaaaaaaa aaaaaaa

```

Fig 7a

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```

1  gggcagcgc gccgcgggct gctgcgctg cgccccgcac cctccccggg cagcagtcog agggccccgc gcgtcccota accatgctgg
   >>CDS.>
   m 1
91  tagcaacgct tctttgcgcg ctctgttgcg gcctctcggc cggctccgct cagctggct actcgaaga cagctgcagc tggaggggca
   >.....CDS.....>
   v a t l i c a l c c g l l a s a h a g y s e d r c s w r g
181  gcggtttgac ccaggagcct ggcagcgtg ggcagctgac cctggactgt actgaggcg ctatcgagt gctgtaccca gctggggcgc
   >.....CDS.....>
   s g l t q e p g s v g q l t l d c t e g a l e w l y p a g a
271  tgcgcctgac cctggggcgc ccgcatcgg gcacacggcc cagcatcgtc tgcctgcgc cagagggcc cttcgtggt gcccaggtct
   >.....CDS.....>
   l r l t l g g p d p g t r p s i v c l r p e r p f a g a q v
361  tcgtgaacg tatgacggc aatctagat tgctactggc cgaggcccg gacctggctg gggcgcgctg catgcgctg ggtccccgcg
   >.....CDS.....>
   f a e r m t g n l e l l l a e g p d l a g g r c m r w g p r
451  agcgccgagc ccttttcctg caggccacac cacacgcga catcagcgc agattgctg ccttcogtt tgaactgcac gaggaccaac
   >.....CDS.....>
   e r x a l f l q a t p h r d i s r r v a a f r f e l h e d q
541  gtgcagaaat gtctcccag gtccaagtc ttggttgga tgggtcctgc aggcctgca gtgatccga gctcctcctg gctgcatgca
   >.....CDS.....>
   r a e m s p g a q g l g v d g a c r p c s d a e l l l a a c
631  ccagtgatt ttgtatccac gggaccatcc atggggtcgc ccatgacaca gagctgcaag aatcagtcac cactgtggtg gttgctcgtg
   >.....CDS.....>
   t s d f v i h g t i h g v a h d t e l q e s v i t v v a r
721  tcacccgcca gacactgcca ctgttcaagg aaggagctc ggagggcaa ggcggggcct ccattgtac cttgctggc tgtggtgtgc
   >.....CDS.....>
   v i r q t l p l f k e g s s e g q g r a s i r t l l r c g v
811  gtctcggccc aggtccttc ctcttcattg gctggagccg atttgcgaa gctgggctg gctgtgctc ccgcttccaa gattcagcc
   >.....CDS.....>
   x p g p g s f l f m g w s r f g e a w l g c a p r f q e f s
901  gtgtctattc agctgcttc acgaaccatc tcaaccatg tgagatgca ctggactgag agacctgga gaaagccctg gatggacctt
   >.....CDS.....>
   r v y s a a l t t h l n p c e m a l d -
991  ctctcggaga tggggtgttg gggagggtga tgggagggtg ggtgagaagg gctgggctcg gatggcatcc tggtaaccac agtgagctgg
1081  tagaatacta agtaacttgg accataccag ccactagat cctgtcttc tgtggcaggc agcatacca gctctgtgc tgcctcactt
1171  tgtctactct ccagtctgct gcccttctaa cccttcttag cctgtgacc agtgagctca tgtttctc gaattccagg gtgtgtctgg
1261  ggttcagagc aacctgccc tagtttgaa gacttgagct aattgtttt tttttgttg tttttttgtt tgttttaagg tggcctgggg
1351  gggcgggcaa aca

```

Fig 7b

1 atgtctggttag cggcgcttct ctgcgcgctg tgctggggcc tcttggtgc gtcgcctoga gctggctact ccgaggaccg ctgcagctgg aggggcagcg
 >>.....CDS.....>
 101 m l v a a l l c a l c c g l l a a s a r a g y s e d r c s w r g s
 gtttgaccca ggaacctggc agctggggc agctgacct ggattgtact gaggtgcta tcgagtggt gttatccagct ggggcgctgc gcctgactct
 >>.....CDS.....>
 201 g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l r l t
 aggcggctct gatccgggca cgcggccag catcgtctgt ctgcgccaa caaggccctt cgctgtgccc caggtcttcg ctgaacggat ggcggccaac
 >>.....CDS.....>
 301 l g g s d p g t r p s i v c l r p t r p f a g a q v f a e r m a g n
 ctgagttgc tactggcga gggccaaggc ctggctgggg gcgctgcat gcgtgggt cctgcgagc gccagacct tttctgcag gccacggcac
 >>.....CDS.....>
 401 l e l l l a e g q g l a g g r c m r w g p r e r a l f l q a t p
 accgggacat cagccgcaga gttgctgcct tccaattga actgcacgag gaccaacgtg cagaaatgtc tcccaggcc caaggttttg gtgtggatgg
 >>.....CDS.....>
 501 h r d i s r v a a f q f e l h e d q r a e m s p q a q g f g v d
 tgcctgcagg cctgcagtg atgcgagct ccttctgact gcatgcacca gtgactttgt gatccatggg accatccatg ggtctgtcca tgacatggag
 >>.....CDS.....>
 601 g a c r p c s d a e l l l t a c t s d f v i h g t i h g v v h d m e
 ctgcaagaat cagtcacac tgtgtggcc actcgtgtca tccgccagc actgcactg ttccaggagg ggagctcga gggccggggc caggcctccg
 >>.....CDS.....>
 701 l q e s v i t v v a t r v i r q t l p l f q e g s s e g r g q a s
 ttcgtacctt gttgcgctgt ggtgtgcgtc ctggcccagg ctcttctc ttcattggct ggagccgatt tggcgaagct tggctgggct gcgctcccg
 >>.....CDS.....>
 801 v r t l l r c g v r p g p g s f l f m g w s r f g e a w l g c a p
 ctccaagag ttacgcgtg tctattcagc tgctctgcg gccacctca accaatgtga ggtggcactg gactgagaga cctggggagca agccctggat
 >>.....CDS.....>
 901 r f q e f s r v y s a a l a a h l n p c e v a l d -
 ggatcttct ctgggggatgg ggtgttgggg aggggtgata ggggggtggg tgggaagggt gtggctcaga tggcatcctg gtaccacag tgaggtggta
 1001 gaatactaaa taacctggat cacacc

Fig 8

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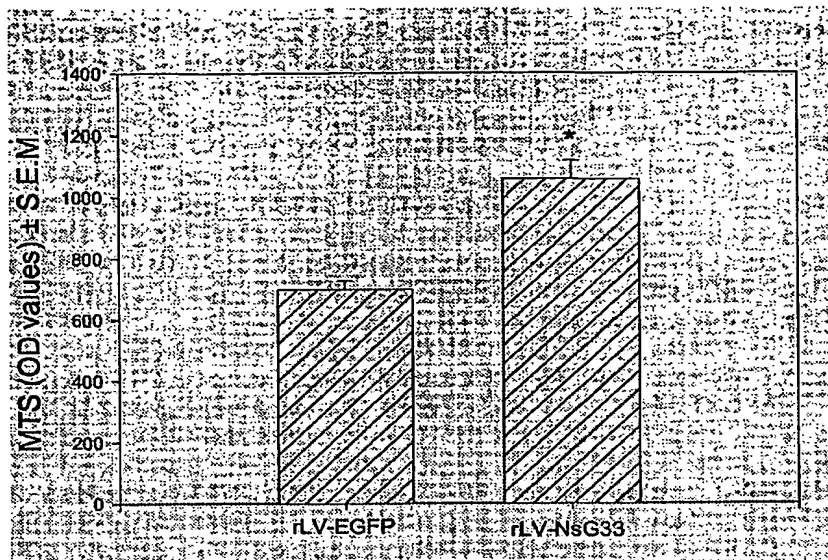


Fig. 9

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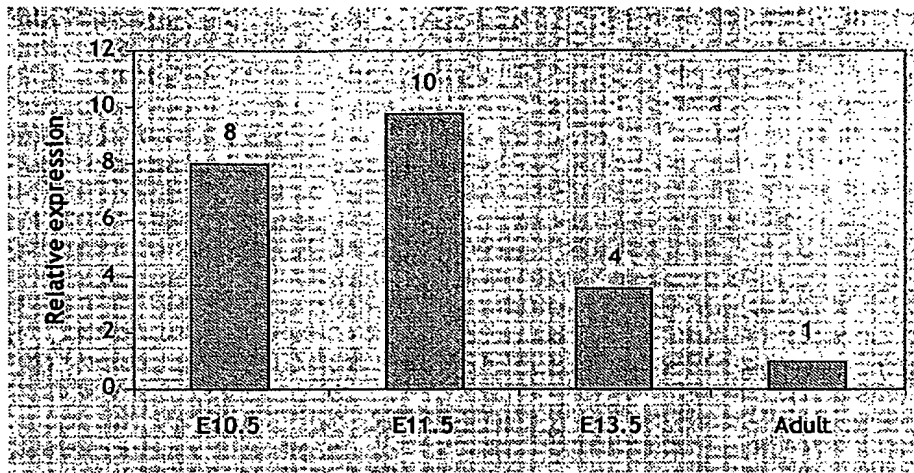


Fig. 10A

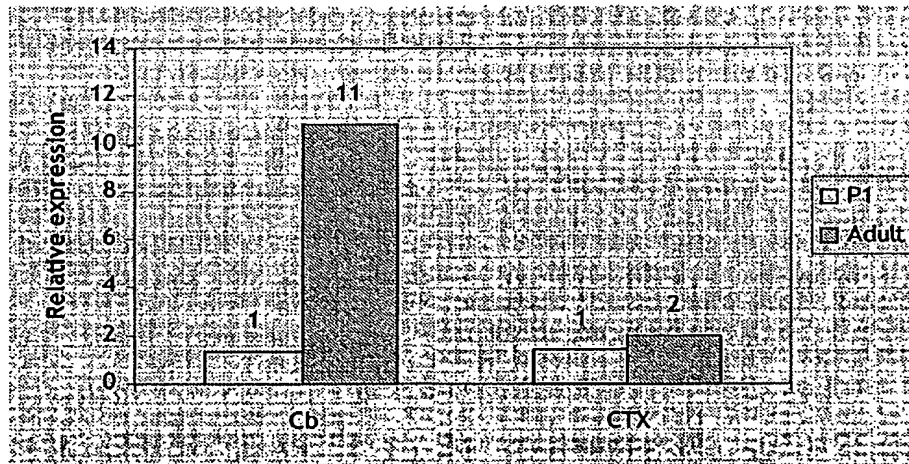


Fig. 10B

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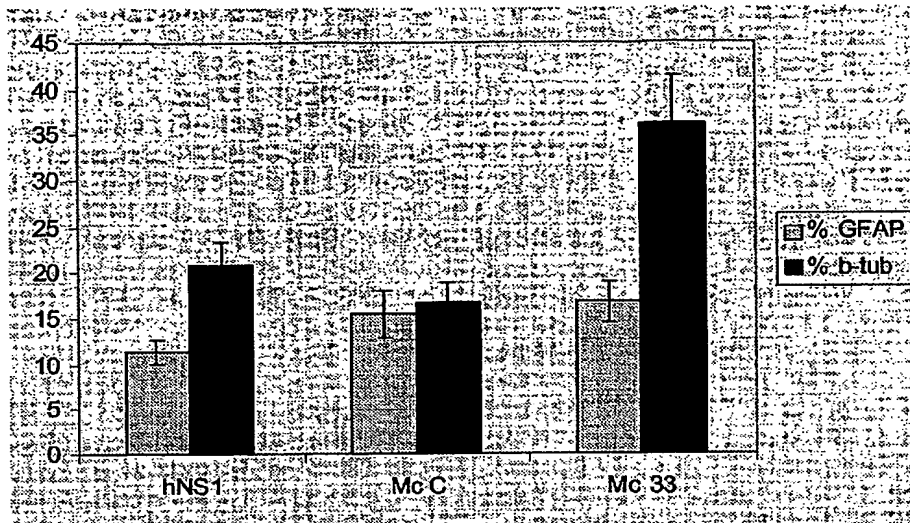


Fig. 11A

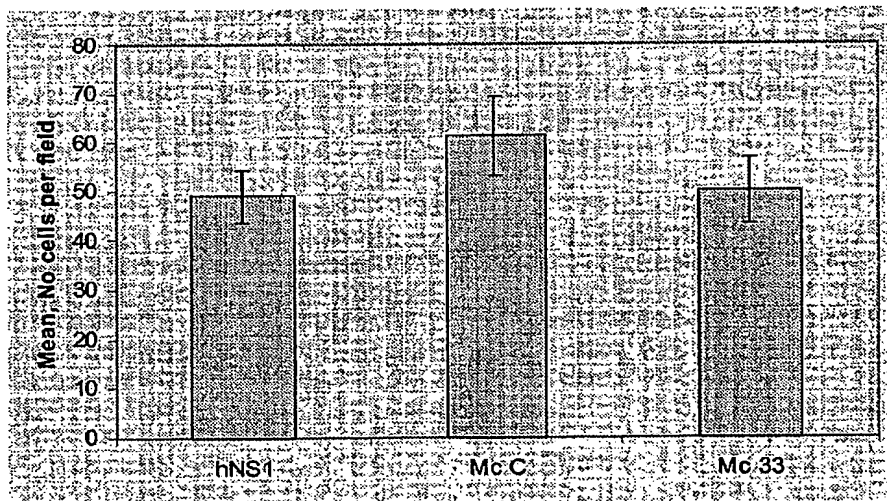


Fig. 11B

f

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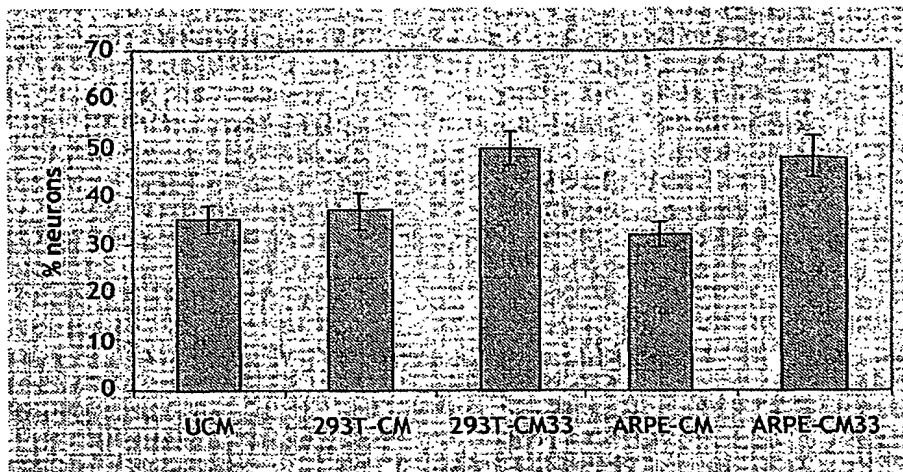


Fig. 12

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- ☒ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

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